

M. DiBriano

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TECH CENTER 1600/2800

1644

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/267,719

DATE: 07/10/2000
TIME: 10:49:01

Input Set : A:\Hs110pl.app
Output Set : N:\CRF3\07102000\I267719.raw

ENTERED

ES

3 <110> APPLICANT: Burks Jr., A. Wesley
4 Helm, Ricki M.
5 Cockrell, Gael
6 Bannon, Gary A.
7 Stanley, J. Steven
8 Shin, David S.
9 Compadre, Cesar M.
10 Huang, Shau-Ku
11 Maleki, Soheila J.
12 Kopper, Randall A.
14 <120> TITLE OF INVENTION: Tertiary Structure of Peanut Allergen ARA H 1
16 <130> FILE REFERENCE: HS 110
18 <140> CURRENT APPLICATION NUMBER: 09/267,719
19 <141> CURRENT FILING DATE: 1999-03-11
21 <150> PRIOR APPLICATION NUMBER: 60/077,763
22 <151> PRIOR FILING DATE: 1998-03-13
24 <160> NUMBER OF SEQ ID NOS: 13
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 626
30 <212> TYPE: PRT
31 <213> ORGANISM: Arachis hypogaea
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37 Leu Ala Ser Val Ser Ala Thr His Ala Lys Ser Ser Pro Tyr Gln Lys
38 20 25 30
40 Lys Thr Glu Asn Pro Cys Ala Gln Arg Cys Leu Gln Ser Cys Gln Gln
41 35 40 45
43 Glu Pro Asp Asp Leu Lys Gln Lys Ala Cys Glu Ser Arg Cys Thr Lys
44 50 55 60
46 Leu Glu Tyr Asp Pro Arg Leu Val Tyr Asp Pro Arg Gly His Thr Gly
47 65 70 75 80
49 Thr Thr Asn Gln Arg Ser Pro Pro Gly Glu Arg Thr Arg Gly Arg Gln
50 85 90 95
52 Pro Gly Asp Tyr Asp Asp Arg Arg Gln Pro Arg Arg Glu Glu Gly
53 100 105 110
55 Gly Arg Trp Gly Pro Ala Gly Pro Arg Glu Arg Glu Arg Glu Glu Asp
56 115 120 125
58 Trp Arg Gln Pro Arg Glu Asp Trp Arg Arg Pro Ser His Gln Gln Pro
59 130 135 140
61 Arg Lys Ile Arg Pro Glu Gly Arg Glu Gly Glu Gln Glu Trp Gly Thr
62 145 150 155 160
64 Pro Gly Ser His Val Arg Glu Glu Thr Ser Arg Asn Asn Pro Phe Tyr
65 165 170 175
67 Phe Pro Ser Arg Arg Phe Ser Thr Arg Tyr Gly Asn Gln Asn Gly Arg
68 180 185 190

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Output Set: N:\CRF3\07102000\I267719.raw

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70 Ile Arg Val Leu Gln Arg Phe Asp Gln Arg Ser Arg Gln Phe Gln Asn
71      195      200      205
73 Leu Gln Asn His Arg Ile Val Gln Ile Glu Ala Lys Pro Asn Thr Leu
74      210      215      220
76 Val Leu Pro Lys His Ala Asp Ala Asp Asn Ile Leu Val Ile Gln Gln
77 225      230      235      240
79 Gly Gln Ala Thr Val Thr Val Ala Asn Gly Asn Asn Arg Lys Ser Phe
80      245      250      255
82 Asn Leu Asp Glu Gly His Ala Leu Arg Ile Pro Ser Gly Phe Ile Ser
83      260      265      270
85 Tyr Ile Leu Asn Arg His Asp Asn Gln Asn Leu Arg Val Ala Lys Ile
86      275      280      285
88 Ser Met Pro Val Asn Thr Pro Gly Gln Phe Glu Asp Phe Pro Ala
89      290      295      300
91 Ser Ser Arg Asp Gln Ser Ser Tyr Leu Gln Gly Phe Ser Arg Asn Thr
92 305      310      315      320
94 Leu Glu Ala Ala Phe Asn Ala Glu Phe Asn Glu Ile Arg Arg Val Leu
95      325      330      335
97 Leu Glu Glu Asn Ala Gly Gly Glu Gln Glu Glu Arg Gly Gln Arg Arg
98      340      345      350
100 Trp Ser Thr Arg Ser Ser Glu Asn Asn Glu Gly Val Ile Val Lys Val
101      355      360      365
103 Ser Lys Glu His Val Glu Glu Leu Thr Lys His Ala Lys Ser Val Ser
104      370      375      380
106 Lys Lys Gly Ser Glu Glu Glu Gly Asp Ile Thr Asn Pro Ile Asn Leu
107 385      390      395      400
109 Arg Glu Gly Glu Pro Asp Leu Ser Asn Asn Phe Gly Lys Leu Phe Glu
110      405      410      415
112 Val Lys Pro Asp Lys Lys Asn Pro Gln Leu Gln Asp Leu Asp Met Met
113      420      425      430
115 Leu Thr Cys Val Glu Ile Lys Glu Gly Ala Leu Met Leu Pro His Phe
116      435      440      445
118 Asn Ser Lys Ala Met Val Ile Val Val Val Asn Lys Gly Thr Gly Asn
119      450      455      460
121 Leu Glu Leu Val Ala Val Arg Lys Glu Gln Gln Gln Arg Gly Arg Arg
122 465      470      475      480
124 Glu Glu Glu Glu Asp Glu Asp Glu Glu Glu Gly Ser Asn Arg Glu
125      485      490      495
127 Val Arg Arg Tyr Thr Ala Arg Leu Lys Glu Gly Asp Val Phe Ile Met
128      500      505      510
130 Pro Ala Ala His Pro Val Ala Ile Asn Ala Ser Ser Glu Leu His Leu
131      515      520      525
133 Leu Gly Phe Gly Ile Asn Ala Glu Asn Asn His Arg Ile Phe Leu Ala
134      530      535      540
136 Gly Asp Lys Asp Asn Val Ile Asp Gln Ile Glu Lys Gln Ala Lys Asp
137 545      550      555      560
139 Leu Ala Phe Pro Gly Ser Gly Glu Gln Val Glu Lys Leu Ile Lys Asn
140      565      570      575
142 Gln Lys Glu Ser His Phe Val Ser Ala Arg Pro Gln Ser Gln Ser Gln

```

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Input Set : A:\Hs110pl.app
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```

143          580          585          590
145 Ser Pro Ser Ser Pro Glu Lys Glu Ser Pro Glu Lys Glu Asp Gln Glu
146          595          600          605
148 Glu Glu Asn Gln Gly Gly Lys Gly Pro Leu Leu Ser Ile Leu Lys Ala
149          610          615          620
151 Phe Asn
152 625
155 <210> SEQ ID NO: 2
156 <211> LENGTH: 371
157 <212> TYPE: PRT
158 <213> ORGANISM: Phaseolus vulgaris
160 <400> SEQUENCE: 2
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162 1 5 10 15
164 Lys Asn Gln Tyr Gly His Ile Arg Val Leu Gln Arg Phe Asp Gln Gln
165 20 25 30
167 Ser Lys Arg Leu Gln Asn Leu Glu Asp Tyr Arg Leu Val Glu Phe Arg
168 35 40 45
170 Ser Lys Pro Glu Thr Leu Leu Leu Pro Gln Gln Ala Asp Ala Glu Leu
171 50 55 60
173 Leu Leu Val Val Arg Ser Gly Ser Ala Ile Leu Val Leu Val Lys Pro
174 65 70 75 80
176 Asp Asp Arg Arg Glu Tyr Phe Phe Leu Thr Ser Asp Asn Pro Ile Phe
177 85 90 95
179 Ser Asp His Gln Lys Ile Pro Ala Gly Thr Ile Phe Tyr Leu Val Asn
180 100 105 110
182 Pro Asp Pro Lys Glu Asp Leu Arg Ile Ile Gln Leu Ala Met Pro Val
183 115 120 125
185 Asn Asn Pro Gln Ile His Glu Phe Phe Leu Ser Ser Thr Glu Ala Gln
186 130 135 140
188 Gln Ser Tyr Leu Gln Glu Phe Ser Lys His Ile Leu Glu Ala Ser Phe
189 145 150 155 160
191 Asn Ser Lys Phe Glu Glu Ile Asn Arg Val Leu Phe Glu Glu Glu Gly
192 165 170 175
194 Gln Gln Glu Gly Val Ile Val Asn Ile Asp Ser Glu Gln Ile Lys Glu
195 180 185 190
197 Leu Ser Lys His Ala Lys Ser Ser Arg Lys Ser Leu Ser Lys Gln
198 195 200 205
200 Asp Asn Thr Ile Gly Asn Glu Phe Gly Asn Leu Thr Glu Arg Thr Asp
201 210 215 220
203 Asn Ser Leu Asn Val Leu Ile Ser Ser Ile Glu Met Glu Glu Gly Ala
204 225 230 235 240
206 Leu Phe Val Pro His Tyr Tyr Ser Lys Ala Ile Val Ile Leu Val Val
207 245 250 255
209 Asn Glu Gly Glu Ala His Val Glu Leu Val Gly Pro Lys Gly Asn Lys
210 260 265 270
212 Glu Thr Leu Glu Tyr Glu Ser Tyr Arg Ala Glu Leu Ser Lys Asp Asp
213 275 280 285
215 Val Phe Val Ile Pro Ala Ala Tyr Pro Val Ala Ile Lys Ala Thr Ser

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TIME: 10:49:01

Input Set : A:\Hs110pl.app

Output Set: N:\CRF3\07102000\I267719.raw

```

216      290      295      300
218 Asn Val Asn Phe Thr Gly Phe Gly Ile Asn Ala Asn Asn Asn Arg
219 305      310      315      320
221 Asn Leu Leu Ala Gly Lys Thr Asp Asn Val Ile Ser Ser Ile Gly Arg
222      325      330      335
224 Ala Leu Asp Gly Lys Asp Val Leu Gly Leu Thr Phe Ser Gly Ser Gly
225      340      345      350
227 Asp Glu Val Met Lys Leu Ile Asn Lys Gln Ser Gly Ser Tyr Phe Val
228      355      360      365
230 Asp Ala His
231      370
234 <210> SEQ ID NO: 3
235 <211> LENGTH: 510
236 <212> TYPE: PRT
237 <213> ORGANISM: Arachis hypogaea
239 <400> SEQUENCE: 3
240 Ile Ser Phe Arg Gln Gln Pro Glu Glu Asn Ala Cys Gln Phe Gln Arg
241 1      5      10      15
243 Leu Asn Ala Gln Arg Pro Asp Asn Arg Ile Glu Ser Glu Gly Gly Tyr
244      20      25      30
246 Ile Glu Thr Trp Asn Pro Asn Asn Gln Glu Phe Glu Cys Ala Gly Val
247      35      40      45
249 Ala Leu Ser Arg Leu Val Leu Arg Arg Asn Ala Leu Arg Arg Pro Phe
250      50      55      60
252 Tyr Ser Asn Ala Pro Gln Glu Ile Phe Ile Gln Gln Gly Arg Gly Tyr
253 65      70      75      80
255 Phe Gly Leu Ile Phe Pro Gly Cys Pro Arg His Tyr Glu Glu Pro His
256      85      90      95
258 Thr Gln Gly Arg Arg Ser Gln Ser Gln Arg Pro Pro Arg Arg Leu Gln
259      100      105      110
261 Gly Glu Asp Gln Ser Gln Gln Gln Arg Asp Ser His Gln Lys Val His
262      115      120      125
264 Arg Phe Asp Glu Gly Asp Leu Ile Ala Val Pro Thr Gly Val Ala Phe
265      130      135      140
267 Trp Leu Tyr Asn Asp His Asp Thr Asp Val Val Ala Val Ser Leu Thr
268 145      150      155      160
270 Asp Thr Asn Asn Asn Asp Asn Gln Leu Asp Gln Phe Pro Arg Arg Phe
271      165      170      175
273 Asn Leu Ala Gly Asn Thr Glu Gln Glu Phe Leu Arg Tyr Gln Gln Gln
274      180      185      190
276 Ser Arg Gln Ser Arg Arg Arg Ser Leu Pro Tyr Ser Pro Tyr Ser Pro
277      195      200      205
279 Gln Ser Gln Pro Arg Gln Glu Glu Arg Glu Phe Ser Pro Pro Arg Gly Gln
280      210      215      220
282 His Ser Arg Arg Glu Arg Ala Gly Gln Glu Glu Glu Asn Glu Gly Gly
283 225      230      235      240
285 Asn Ile Phe Ser Gly Phe Thr Pro Glu Phe Leu Glu Gln Ala Phe Gln
286      245      250      255
288 Val Asp Asp Arg Gln Ile Val Gln Asn Leu Arg Gly Glu Thr Glu Ser

```

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```

289          260          265          270
291 Glu Glu Glu Gly Ala Ile Val Thr Val Arg Gly Gly Leu Arg Ile Leu
292          275          280          285
294 Ser Pro Asp Arg Lys Arg Arg Ala Asp Glu Glu Glu Glu Tyr Asp Glu
295          290          295          300
297 Asp Glu Tyr Glu Tyr Asp Glu Glu Asp Arg Arg Gly Arg Gly Ser
298 305          310          315          320
300 Arg Gly Arg Gly Asn Gly Ile Glu Glu Thr Ile Cys Thr Ala Ser Ala
301          325          330          335
303 Lys Lys Asn Ile Gly Arg Asn Arg Ser Pro Asp Ile Tyr Asn Pro Gln
304          340          345          350
306 Ala Gly Ser Leu Lys Thr Ala Asn Asp Leu Asn Leu Leu Ile Leu Arg
307          355          360          365
309 Trp Leu Gly Leu Ser Ala Glu Tyr Gly Asn Leu Tyr Arg Asn Ala Leu
310          370          375          380
312 Phe Val Ala His Tyr Asn Thr Asn Ala His Ser Ile Ile Tyr Arg Leu
313 385          390          395          400
315 Arg Gly Arg Ala His Val Gln Val Val Asp Ser Asn Gly Asn Arg Val
316          405          410          415
318 Tyr Asp Glu Glu Leu Gln Glu Gly His Val Leu Val Val Pro Gln Asn
319          420          425          430
321 Phe Ala Val Ala Gly Lys Ser Gln Ser Glu Asn Phe Glu Tyr Val Ala
322          435          440          445
324 Phe Lys Thr Asp Ser Arg Pro Ser Ile Ala Asn Leu Ala Gly Glu Asn
325          450          455          460
327 Ser Val Ile Asp Asn Leu Pro Glu Glu Val Val Ala Asn Ser Tyr Gly
328 465          470          475          480
330 Leu Gln Arg Glu Gln Ala Arg Gln Leu Lys Asn Asn Asn Pro Phe Lys
331          485          490          495
333 Phe Phe Val Pro Ser Gln Gln Ser Pro Arg Ala Val Ala
334          500          505          510
337 <210> SEQ ID NO: 4
338 <211> LENGTH: 473
339 <212> TYPE: PRT
340 <213> ORGANISM: Glycine max
342 <400> SEQUENCE: 4
343 Met Ala Ser Lys Val Val Ser Val Leu Val Ile Ala Met Met Leu Phe
344 1          5          10          15
346 Ala Met Asn Cys Asn Cys Thr Ser Val Gly His Met Pro Ser Thr Lys
347          20          25          30
349 Glu Glu Gly His Asp Phe Gln Glu Ser Lys Ala Lys Thr Thr Gln Thr
350          35          40          45
352 Ala Asn Lys Ala Met Glu Thr Gly Lys Glu Gly Gln Glu Ala Ala Glu
353          50          55          60
355 Ser Trp Thr Glu Trp Ala Lys Glu Lys Leu Ser Glu Gly Leu Gly Phe
356 65          70          75          80
358 Lys His Asp Gln Glu Ser Lys Glu Ser Thr Thr Asn Lys Val Ser Asp
359          85          90          95
361 Tyr Ala Thr Asp Thr Ala Gln Lys Ser Lys Asp Tyr Ala Thr Asp Thr

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 07/10/2000

PATENT APPLICATION: US/09/267,719

TIME: 10:49:02

Input Set : A:\Hs110pl.app

Output Set: N:\CRF3\07102000\I267719.raw

L:476 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:476 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:476 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:523 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:523 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:523 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:526 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:526 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:595 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:595 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:595 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:598 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:598 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
M:340 Repeated in SeqNo=7
L:826 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:826 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:826 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:826 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:826 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10